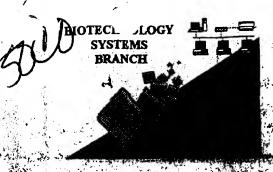
RAW SEQUENCE LISTING ERROR REPORT



#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center 18 FIG. detected errors when processing the following computer readable

Application Secul Number: 69/86/00f

Source 69/86/00f

7/9/00

HAVE TABLE PROTOUT EXPLAINS DETECTED ERRORS.

HAVE TO BE THE DEPORTMENT OF THE APPLICANT BY ETHER:

LIFE OF THE PRINTOUT IN YOUR NEXT COMMUNICATION TO THE PRINTOUT WITHER OF THE PRINTOUT WITHER.

LIFE OF THE PRINTOUT WITHER OF THE PRINTOUT WITHER.

LIFE OF THE PRINTOUT WITHER.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX: 703-308-4216.

PATENTIN 2:1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

6

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/869,004
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers, use space characters, instead
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules Please ensure your subsequent submission is saved in ASCII text.
SVariable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0	A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)
7Skipped Sequences (OLD RULES)	Sequence(s) missing If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION SEQ ID NO.X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
•	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
8Skipped Sequences (NEW RULES)	Sequence(s) missing If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
1	Sequence(s)missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
"bue"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk

AMC -- Biotechnology Systems Branch -- 06/04/2001

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,004

DATE: 07/09/2001 TIME: 10:11:50

Input Set : A:\Ru-0076.app

Output Set: N:\CRF3\07092001\1869004.raw

```
, see next page
      3/140> CURRENT APPLICATION NUMBER: US/09/869,004
                                                                          Does Not Comply
      $ <141> CURRENT FILING DATE: 2001-06-22
                                                                      Corrected Diskette Needea
     0 <110> APPLICANT:
W--> \int 0 <120> TITLE INVENTION:
W--> 0 <130> FILE REFERENCE:
      0 ::150 FRIOR APPLICATION NUMBER: 60/113,731
      4 0151 FFIOF FILING DATE: 1998-12-23
      0 1100: NUMBER OF SEQ ID NOS: 3
      8 (17) SOFTWARE: PatentIn Ver. 2.0
     10 <210 SEQ 10 NO: 1
     11 (211 IEUGTH: 13
     12 H212H TYPE: DNA
     13 - 213: OFGANISM: Artificial Sequence
     15 KILON FEATURE:
     16 :2130 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
     18 - 3400% SEQUENCE: 1
                                                                             13
     19 quistacabat dog
     21 42102 SEQ ID NO: 2
     21 H211 IFFGTH: 13
     ES FEILE TYPE: ENA
     24 02230 OFGANISM: Artificial Sequence
     26 MIO: FEATURE:
     27 (2.3) OTHER INFORMATION: Description of Artificial Sequence: Synthetic
     HM -:4100: SEQUENCE: 2
                                                                             13
     30 ogdatgtgta ogd
     32 H2107 SEQ ID NO: 3
     33 U.11 LEDGTH: 13
     34 KINIZ TYPE: DNA
        1213 - 05GANISM: Artificial Sequence
        CLES OTHER INFORMATION: Description of Artificial Sequence: Synthetic Julius
     37 WALDON FEATURE:
             n basic furan
     3:4
     41 GULOS FEATURES
     41: (127) NAME/REY: misc_feature

13 (1200) LOCATION: (7)

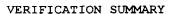
45 (400) SEQUENCE: 5

46 cgcatgngta cgc

13 On the Own

C2237 line
W--> 46 cgcatgngta cgc
```

FYI: "n" can only represent a single revelentide (base), hothing ilve



PATENT APPLICATION: US/09/869,004

DATE: 07/09/2001 TIME: 10:11:51

Input Set : A:\Ru-0076.app

Output Set: N:\CRF3\07092001\1869004.raw

L:3 M:270 C: Current Application Number differs, Replaced Current Application No

L:3 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, APPLICANT NAME L:0 M:201 W: Mandatory field data missing, TITLE INVENTION L:0 M:201 W: Mandatory field data missing, FILE REFERENCE

L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID\$#:3